

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1565.6	73.8	2247	6	AK167460	AK167460 Mus muscu
2	1564	73.8	2269	6	AK077740	AK077740 Mus muscu
3	754.2	35.6	760	8	CO565622	CO565622 AGENCOURT
4	699.2	33.0	790	8	CO572777	CO572777 AGENCOURT
5	690.8	32.6	782	8	CO574051	CO574051 AGENCOURT
6	679.8	32.1	794	8	CO567769	CO567769 AGENCOURT
7	664.4	31.3	1317	10	DV789420	DV789420 Hw_liver_
8	634.8	29.9	808	8	CO573278	CO573278 AGENCOURT
9	632	29.8	886	5	CF551083	CF551083 AGENCOURT
10	631.2	29.8	738	8	CO574740	CO574740 AGENCOURT
11	625.2	29.5	793	2	BI217680	BI217680 602934527
12	597.8	28.2	840	10	DV813743	DV813743 LB01711.C
13	596.4	28.1	744	8	CV114224	CV114224 AGENCOURT
14	592.4	27.9	594	8	CO556968	CO556968 AGENCOURT
15	580.2	27.4	792	8	CO425730	CO425730 UI-M-HU0-
16	579.6	27.3	867	2	BI218342	BI218342 602937723
17	578.8	27.3	758	9	DN119973	DN119973 1119949 M
18	573.6	27.1	872	4	CA752105	CA752105 UI-M-FD0-
19	573.4	27.0	735	10	DT889191	DT889191 1466050 M
20	569.8	26.9	797	1	AI097875	AI097875 ue40h10.y
21	563	26.6	670	2	BI331204	BI331204 602985159
22	549.8	25.9	831	8	CO567345	CO567345 AGENCOURT
23	549.2	25.9	618	8	CN724649	CN724649 E0883A09-
24	546.4	25.8	821	3	BP442620	BP442620 BP442620
25	538.4	25.4	886	3	BQ946437	BQ946437 AGENCOURT
c 26	536.2	25.3	840	9	DN120322	DN120322 1120333 M
27	528.4	24.9	719	2	BI146400	BI146400 602910767
28	526.4	24.8	951	7	BF533689	BF533689 602074093
c 29	522	24.6	682	4	CB421561	CB421561 594587 MA
30	521.4	24.6	728	2	BI145731	BI145731 602909885
31	519.6	24.5	770	2	BI149152	BI149152 602914216
32	514	24.2	826	2	BI731492	BI731492 603354382
33	498.2	23.5	949	4	BX849476	BX849476 BX849476
34	497.4	23.5	962	7	BF233498	BF233498 602024290
c 35	495	23.3	578	8	CO560193	CO560193 AGENCOURT
36	492	23.2	645	9	DN129329	DN129329 1143472 M
37	491.2	23.2	746	8	CO570899	CO570899 AGENCOURT
38	487.6	23.0	740	2	BI145941	BI145941 602911272
39	486.6	23.0	763	4	CB949170	CB949170 AGENCOURT
40	484.2	22.8	778	2	BI146017	BI146017 602911373
41	481.4	22.7	749	10	DV812815	DV812815 LB0147.CR
42	481.2	22.7	1036	7	BF533289	BF533289 602073744
43	475.4	22.4	956	2	BI328145	BI328145 602985402
44	474.6	22.4	665	3	BQ109198	BQ109198 imageqc_6
45	470.6	22.2	726	10	DT723071	DT723071 LB0142.CR

ALIGNMENTS

RESULT 1

AK167460

LOCUS

AK167460

2247 bp

mRNA

linear

HTC 21-SEP-2005

SCORE Search Results Details for Application 10606302 and Search Result us-10-606-302a- 10.rnpbn.

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OM nucleic - nucleic search, using sw model

Run on: August 15, 2006, 14:38:19 ; Search time 393.828 Seconds
(without alignments)
8548.706 Million cell updates/sec

Title: US-10-606-302A-10
Perfect score: 2120
Sequence: 1 ggatcctcctgatcactgga.....accaagatgttccagctacc 2120

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2200221 seqs, 794037843 residues

Total number of hits satisfying chosen parameters: 4400442

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_NA_New:*

- 1: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09_NEW_PUB.seq:*
- 2: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US06_NEW_PUB.seq:*
- 3: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US07_NEW_PUB.seq:*
- 4: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US08_NEW_PUB.seq:*
- 5: /EMC_Celerra_SIDS3/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
- 6: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10_NEW_PUB.seq:*
- 7: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11_NEW_PUB.seq:*
- 8: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11_NEW_PUB.seq1:*
- 9: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11_NEW_PUB.seq2:*
- 10: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US60_NEW_PUB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	Score	% Match	Query Length	DB	ID	Description
No.						
1	470.4	22.2	668	6	US-10-488-619-2085	Sequence 2085, Ap
2	466.8	22.0	510	6	US-10-488-619-2087	Sequence 2087, Ap
c 3	365.4	17.2	791	6	US-10-488-619-2086	Sequence 2086, Ap
c 4	346	16.3	733	6	US-10-488-619-2084	Sequence 2084, Ap
5	90.8	4.3	2152	6	US-10-449-902-27255	Sequence 27255, A
6	84.4	4.0	2420	9	US-11-218-305-19629	Sequence 19629, A
7	77.4	3.7	1581	8	US-11-217-529-1906	Sequence 1906, Ap
8	73.8	3.5	1581	8	US-11-217-529-77873	Sequence 77873, A
9	45.4	2.1	1561	6	US-10-449-902-6166	Sequence 6166, Ap
10	45.4	2.1	1740	6	US-10-449-902-6130	Sequence 6130, Ap
c 11	44.6	2.1	2741	9	US-11-218-305-22630	Sequence 22630, A
c 12	42.6	2.0	1234	6	US-10-449-902-6007	Sequence 6007, Ap
13	42.6	2.0	2059	6	US-10-449-902-8518	Sequence 8518, Ap
14	42.2	2.0	2120	8	US-11-266-748A-70478	Sequence 70478, A
15	42.2	2.0	2120	8	US-11-266-748A-106039	Sequence 106039,
c 16	42.2	2.0	2120	8	US-11-266-748A-123289	Sequence 123289,
17	41.8	2.0	1176	8	US-11-217-529-81002	Sequence 81002, A
c 18	41.2	1.9	2133	9	US-11-348-413-1505	Sequence 1505, Ap
19	41	1.9	1334	6	US-10-449-902-21405	Sequence 21405, A
20	39.8	1.9	657	8	US-11-266-748A-163252	Sequence 163252,
c 21	39.6	1.9	787	8	US-11-266-748A-175933	Sequence 175933,
22	39.6	1.9	1672	6	US-10-449-902-15918	Sequence 15918, A
23	39.2	1.8	1658	9	US-11-174-307B-3883	Sequence 3883, Ap
24	39	1.8	2087	6	US-10-449-902-9658	Sequence 9658, Ap
25	38.8	1.8	741	6	US-10-374-780A-1007	Sequence 1007, Ap
26	38.8	1.8	4453	9	US-11-218-305-17561	Sequence 17561, A
27	38.4	1.8	936	8	US-11-266-748A-60691	Sequence 60691, A
28	38.4	1.8	1000	8	US-11-266-748A-290001	Sequence 290001,
c 29	38.4	1.8	1000	8	US-11-266-748A-341430	Sequence 341430,
30	38.4	1.8	1307	8	US-11-266-748A-258261	Sequence 258261,
c 31	38.4	1.8	1307	8	US-11-266-748A-318778	Sequence 318778,
c 32	38.4	1.8	2412	8	US-11-266-748A-258884	Sequence 258884,
33	38.4	1.8	2412	8	US-11-266-748A-319401	Sequence 319401,
34	38.4	1.8	2427	9	US-11-384-733-2	Sequence 2, Appli
c 35	38.4	1.8	5338	8	US-11-266-748A-29879	Sequence 29879, A
c 36	38.2	1.8	2154	9	US-11-218-305-23430	Sequence 23430, A
37	38	1.8	1529	9	US-11-218-305-14820	Sequence 14820, A
38	37.8	1.8	1381	9	US-11-056-355B-12335	Sequence 12335, A
39	37.8	1.8	1452	9	US-11-218-305-1646	Sequence 1646, Ap
40	37.6	1.8	913	8	US-11-266-748A-161902	Sequence 161902,
41	37.6	1.8	8404	8	US-11-266-748A-28705	Sequence 28705, A
42	37.6	1.8	8833	6	US-10-505-928-785	Sequence 785, App
43	37.6	1.8	8833	8	US-11-266-748A-29245	Sequence 29245, A
44	37.6	1.8	8833	8	US-11-266-748A-31810	Sequence 31810, A
45	37.6	1.8	8833	8	US-11-266-748A-56209	Sequence 56209, A

ALIGNMENTS

RESULT 1

US-10-488-619-2085

; Sequence 2085, Application US/10488619

; Publication No. US20060099578A1

; GENERAL INFORMATION:

; APPLICANT: Greenlee, Winner and Sullivan, P.C.

; TITLE OF INVENTION: Human Mitochondrial DNA Polymorphisms, Haplogroups, Association

SCORE Search Results Details for Application 10606302 and Search Result us-10-606-302a-10.rnpbm

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OM nucleic - nucleic search, using sw model

Run on: August 15, 2006, 13:10:24 ; Search time 2658.71 Seconds
(without alignments)
9797.893 Million cell updates/sec

Title: US-10-606-302A-10
Perfect score: 2120
Sequence: 1 ggatcctcctgatcactgga.....accaagatgttccagctacc 2120

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 18892170 seqs, 6143817638 residues

Total number of hits satisfying chosen parameters: 37784340

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_NA_Main:*

- 1: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US07_PUBCOMB.seq:*
- 2: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US08_PUBCOMB.seq:*
- 3: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09A_PUBCOMB.seq:*
- 4: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09B_PUBCOMB.seq:*
- 5: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09C_PUBCOMB.seq:*
- 6: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10A_PUBCOMB.seq:*
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- 8: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10C_PUBCOMB.seq:*
- 9: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10D_PUBCOMB.seq:*
- 10: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10E_PUBCOMB.seq:*
- 11: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10F_PUBCOMB.seq:*
- 12: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10G_PUBCOMB.seq:*
- 13: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11A_PUBCOMB.seq:*
- 14: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11B_PUBCOMB.seq:*
- 15: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11C_PUBCOMB.seq:*
- 16: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11D_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed,

and is derived by analysis of the total score distribution.

SUMMARIES

Result	Score	% Query Match	Length	DB	ID	Description
No.						
1	2120	100.0	2120	9	US-10-606-300-10	Sequence 10, Appl
2	2120	100.0	2120	10	US-10-606-302-10	Sequence 10, Appl
3	1323	62.4	1323	3	US-09-917-800A-1694	Sequence 1694, Ap
4	592	27.9	688	8	US-10-404-460-106	Sequence 106, App
c 5	324	15.3	384	3	US-09-917-800A-659	Sequence 659, App
6	203.6	9.6	242	3	US-09-960-352-12740	Sequence 12740, A
c 7	169	8.0	201	3	US-09-864-408A-2307	Sequence 2307, Ap
8	164.6	7.8	1317	7	US-10-156-761-2396	Sequence 2396, Ap
9	164.6	7.8	9025608	7	US-10-156-761-1	Sequence 1, Appli
10	120.4	5.7	1284	3	US-09-894-844-106	Sequence 106, App
11	120.4	5.7	1284	8	US-10-388-902-106	Sequence 106, App
12	120.4	5.7	1284	8	US-10-647-089-106	Sequence 106, App
13	120.4	5.7	1284	16	US-11-143-401-106	Sequence 106, App
14	118	5.6	248	8	US-10-430-201-3718	Sequence 3718, Ap
15	118	5.6	248	8	US-10-430-201-3719	Sequence 3719, Ap
16	111	5.2	128	7	US-10-388-934-131	Sequence 131, App
17	111	5.2	128	16	US-11-224-663-131	Sequence 131, App
18	111	5.2	128	16	US-11-224-525-131	Sequence 131, App
c 19	98	4.6	1000	10	US-10-750-185-41341	Sequence 41341, A
c 20	98	4.6	1000	10	US-10-750-623-41341	Sequence 41341, A
21	94.4	4.5	2034	6	US-10-234-026-12	Sequence 12, Appl
22	94.4	4.5	2064	9	US-10-606-300-4	Sequence 4, Appli
23	94.4	4.5	2064	10	US-10-606-302-4	Sequence 4, Appli
24	92.4	4.4	2142	8	US-10-437-963-16021	Sequence 16021, A
25	84.4	4.0	3069	9	US-10-425-115-63810	Sequence 63810, A
26	78.2	3.7	1833	9	US-10-606-300-2	Sequence 2, Appli
27	78.2	3.7	1833	10	US-10-606-302-2	Sequence 2, Appli
28	77.4	3.7	1581	11	US-10-932-182A-1906	Sequence 1906, Ap
29	73.8	3.5	1581	9	US-10-606-300-6	Sequence 6, Appli
30	73.8	3.5	1581	10	US-10-606-302-6	Sequence 6, Appli
31	73.8	3.5	1581	11	US-10-932-182A-77873	Sequence 77873, A
32	73.8	3.5	2138	9	US-10-606-300-8	Sequence 8, Appli
33	73.8	3.5	2138	10	US-10-606-302-8	Sequence 8, Appli
34	73	3.4	1066	8	US-10-424-599-24226	Sequence 24226, A
35	64.4	3.0	409	12	US-10-301-480-273360	Sequence 273360,
36	64.4	3.0	409	12	US-10-301-480-886769	Sequence 886769,
37	64.4	3.0	420	4	US-09-925-065A-182834	Sequence 182834,
38	64.4	3.0	420	5	US-09-925-065A-182834	Sequence 182834,
39	61.8	2.9	321	3	US-09-770-517C-7	Sequence 7, Appli
40	61.8	2.9	321	8	US-10-750-026-7	Sequence 7, Appli
41	55.4	2.6	696	8	US-10-767-701-2324	Sequence 2324, Ap
42	54.2	2.6	1266	7	US-10-156-761-2078	Sequence 2078, Ap
c 43	52.2	2.5	545	6	US-10-027-632-5229	Sequence 5229, Ap
c 44	52.2	2.5	545	7	US-10-027-632-5229	Sequence 5229, Ap
45	51.4	2.4	532	6	US-10-027-632-57456	Sequence 57456, A

ALIGNMENTS

RESULT 1

US-10-606-300-10

; Sequence 10, Application US/10606300

; Publication No. US20050019879A1

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OM nucleic - nucleic search, using sw model

Run on: August 15, 2006, 11:29:45 ; Search time 277.821 Seconds
(without alignments)
14278.103 Million cell updates/sec

Title: US-10-606-302A-10
Perfect score: 2120
Sequence: 1 ggatcctcctgatcactgga.....accaagatgttccagctacc 2120

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1403666 seqs, 935554401 residues

Total number of hits satisfying chosen parameters: 2807332

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_NA:*

- 1: /EMC_Celerra_SIDS3/ptodata/2/ina/1_COMB.seq:*
- 2: /EMC_Celerra_SIDS3/ptodata/2/ina/5_COMB.seq:*
- 3: /EMC_Celerra_SIDS3/ptodata/2/ina/6A_COMB.seq:*
- 4: /EMC_Celerra_SIDS3/ptodata/2/ina/6B_COMB.seq:*
- 5: /EMC_Celerra_SIDS3/ptodata/2/ina/7_COMB.seq:*
- 6: /EMC_Celerra_SIDS3/ptodata/2/ina/H_COMB.seq:*
- 7: /EMC_Celerra_SIDS3/ptodata/2/ina/PCTUS_COMB.seq:*
- 8: /EMC_Celerra_SIDS3/ptodata/2/ina/PP_COMB.seq:*
- 9: /EMC_Celerra_SIDS3/ptodata/2/ina/RE_COMB.seq:*
- 10: /EMC_Celerra_SIDS3/ptodata/2/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB	ID	Description
1	2120	100.0	2120	3	US-09-630-983A-10	Sequence 10, Appl
2	120.4	5.7	1284	3	US-09-894-844-106	Sequence 106, App
3	120.4	5.7	1932	3	US-09-252-991A-7271	Sequence 7271, Ap
4	120.4	5.7	4403765	3	US-09-103-840A-2	Sequence 2, Appli
5	120.4	5.7	4411529	3	US-09-103-840A-1	Sequence 1, Appli
c 6	101.8	4.8	1392	3	US-09-252-991A-7430	Sequence 7430, Ap
7	94.4	4.5	2034	3	US-09-423-468A-12	Sequence 12, Appl
8	94.4	4.5	2064	3	US-09-630-983A-4	Sequence 4, Appli
9	78.2	3.7	1833	3	US-09-630-983A-2	Sequence 2, Appli
10	73.8	3.5	1581	3	US-09-630-983A-6	Sequence 6, Appli
11	73.8	3.5	2138	3	US-09-630-983A-8	Sequence 8, Appli
12	61.8	2.9	321	3	US-09-770-517C-7	Sequence 7, Appli
13	61.8	2.9	321	3	US-10-750-026-7	Sequence 7, Appli
14	60.2	2.8	7218	2	US-08-232-463-14	Sequence 14, Appl
15	51.4	2.4	1185	3	US-09-248-796A-3166	Sequence 3166, Ap
16	45	2.1	1089	3	US-09-252-991A-1313	Sequence 1313, Ap
17	45	2.1	3981	3	US-09-252-991A-1361	Sequence 1361, Ap
c 18	45	2.1	4179	3	US-09-252-991A-1244	Sequence 1244, Ap
19	43.8	2.1	2037	3	US-09-902-540-6164	Sequence 6164, Ap
c 20	43.8	2.1	2039	3	US-09-902-540-304	Sequence 304, App
21	43.2	2.0	3120	3	US-09-423-468A-14	Sequence 14, Appl
22	42.2	2.0	3776	3	US-09-900-237-3	Sequence 3, Appli
23	41.4	2.0	4187	4	US-09-880-107-1609	Sequence 1609, Ap
24	41	1.9	1419	3	US-09-266-965-61	Sequence 61, Appl
25	41	1.9	1499	3	US-09-902-540-6928	Sequence 6928, Ap
26	41	1.9	3465	3	US-09-902-540-596	Sequence 596, App
c 27	41	1.9	53500	3	US-09-266-965-76	Sequence 76, Appl
28	40.6	1.9	1566	3	US-09-252-991A-1548	Sequence 1548, Ap
c 29	40.6	1.9	1611	3	US-09-252-991A-1569	Sequence 1569, Ap
30	40.6	1.9	2088	3	US-09-252-991A-1453	Sequence 1453, Ap
31	40.6	1.9	3568	3	US-10-160-719A-1	Sequence 1, Appli
32	40.6	1.9	3568	3	US-10-209-059-41	Sequence 41, Appl
33	39.6	1.9	1314	3	US-09-252-991A-16243	Sequence 16243, A
34	39.6	1.9	1500	3	US-09-252-991A-16352	Sequence 16352, A
c 35	39.6	1.9	1584	3	US-09-252-991A-16239	Sequence 16239, A
36	39	1.8	1602	3	US-09-124-541-10	Sequence 10, Appl
37	39	1.8	1602	3	US-09-663-326-10	Sequence 10, Appl
c 38	38.8	1.8	505	3	US-09-621-976-15639	Sequence 15639, A
39	38.4	1.8	1026	3	US-09-902-540-3767	Sequence 3767, Ap
40	38.4	1.8	1185	3	US-09-023-339-3	Sequence 3, Appli
41	38.4	1.8	1185	4	US-10-077-381-14	Sequence 14, Appl
42	38.4	1.8	1260	3	US-09-023-173-5	Sequence 5, Appli
43	38.4	1.8	1308	3	US-09-023-173-10	Sequence 10, Appl
44	38.4	1.8	1308	3	US-09-023-339-6	Sequence 6, Appli
45	38.4	1.8	1664	3	US-09-438-917-5	Sequence 5, Appli

ALIGNMENTS

RESULT 1

US-09-630-983A-10

; Sequence 10, Application US/09630983A

; Patent No. 6630330

; GENERAL INFORMATION:

; APPLICANT: Porro, Danilo

; APPLICANT: Sauer, Michael

**SCORE Search Results Details for Application
10606302 and Search Result us-10-606-302a-
10.rng.**

Comments /
Suggestions

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OM nucleic - nucleic search, using sw model

```
Run on:      August 15, 2006, 09:24:26 ; Search time 1194.93 Seconds
              (without alignments)
              12369.931 Million cell updates/sec
```

```
Title:          US-10-606-302A-10
Perfect score:  2120
Sequence:       1 ggatcctcctgatcactgga.....accaagatgttcagctacc 2120
```

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 5244920 seqs, 3486124231 residues

Total number of hits satisfying chosen parameters: 10489840

```
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
```

```
Post-processing: Minimum Match 0%
                  Maximum Match 100%
                  Listing first 45 summaries
```

```
Database : N_Geneseq_8:*
1:  geneseqn1980s:*
2:  geneseqn1990s:*
3:  geneseqn2000s:*
4:  geneseqn2001as:*
5:  geneseqn2001bs:*
6:  geneseqn2002as:*
7:  geneseqn2002bs:*
8:  geneseqn2003as:*
9:  geneseqn2003bs:*
10: geneseqn2003cs:*
11: geneseqn2003ds:*
12: geneseqn2004as:*
13: geneseqn2004bs:*
14: geneseqn2005s:*
15: geneseqn2006s:*
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result		%					
No.	Score	Query Match	Length	DB	ID	Description	
1	2120	100.0	2120	1	AAN92440	Aan92440 DNA seque	
2	2120	100.0	2120	6	ABK10124	Abk10124 Rat cDNA	
3	1323	62.4	1323	6	ABK63787	Abk63787 Rat seque	
4	1323	62.4	1323	10	ADB58424	Adb58424 Toxicity-	
5	1323	62.4	1323	10	ADB53007	Adb53007 Primary r	
6	1323	62.4	1323	13	ADT71411	Adt71411 Rat L-gul	
7	1319.8	62.3	1323	2	AAT87005	Aat87005 DNA encod	
8	592	27.9	688	6	ABT09006	Abt09006 Phase-1 R	
9	592	27.9	688	10	ADG30926	Adg30926 Liver tox	
10	592	27.9	688	12	ADG45513	Adg45513 Liver inf	
11	592	27.9	688	13	ADR91163	Adr91163 Spleen ne	
12	470.4	22.2	668	10	ADD34307	Add34307 Mouse mit	
13	466.8	22.0	510	10	ADD34309	Add34309 Mouse mit	
c 14	365.4	17.2	791	10	ADD34308	Add34308 Mouse mit	
c 15	346	16.3	733	10	ADD34306	Add34306 Mouse mit	
c 16	324	15.3	384	6	ABK62752	Abk62752 Rat seque	
c 17	324	15.3	384	10	ADB56666	Adb56666 Toxicity-	
18	203.6	9.6	242	8	ABX47575	Abx47575 Bovine ES	
c 19	169	8.0	201	6	ABN76207	Abn76207 Human ORF	
20	156.8	7.4	167	6	ABN16596	Abn16596 Human ORF	
21	120.4	5.7	1284	13	ADR96680	Adr96680 M. tuberc	
22	120.4	5.7	1932	11	ABD08667	Abd08667 Pseudomon	
23	120.4	5.7	110000	4	AAI99682_19	Continuation (20 o	
24	120.4	5.7	110000	4	AAI99682_20	Continuation (21 o	
25	120.4	5.7	110000	4	AAI99683_19	Continuation (20 o	
26	120.4	5.7	110000	4	AAI99683_20	Continuation (21 o	
27	118	5.6	248	12	ADL87326	Adl87326 DNA up-re	
28	118	5.6	248	12	ADL87325	Adl87325 DNA up-re	
29	113.4	5.3	713	6	ABL60142	Abl60142 Fungi str	
30	111	5.2	128	11	ADW21752	Adw21752 Rat hepat	
c 31	101.8	4.8	1392	11	ABD08826	Abd08826 Pseudomon	
32	94.4	4.5	2034	2	AAV69438	Aav69438 Cauliflow	
33	94.4	4.5	2064	6	ABK10121	Abk10121 B. olerac	
34	90.8	4.3	2023	2	AAX31915	Aax31915 L-galacto	
35	78.2	3.7	1833	6	ABK10120	Abk10120 A. thalia	
36	73.8	3.5	1581	6	ABK10122	Abk10122 Yeast cDN	
37	73.8	3.5	1591	4	AAF58029	Aaf58029 S cerevis	
38	73.8	3.5	2138	6	ABK10123	Abk10123 Yeast cDN	
39	65	3.1	1248	2	AAV11297	Aav11297 Nucleotid	
40	63.4	3.0	720	2	AAV11295	Aav11295 N-termina	
41	62.6	3.0	1386	4	AAF76931	Aaf76931 Penicilli	
42	62.6	3.0	1443	4	AAF76930	Aaf76930 Penicilli	
43	62.6	3.0	1774	4	AAF76929	Aaf76929 Penicilli	
44	61.8	2.9	321	4	AAH43266	Aah43266 D-aminoac	
c 45	58.4	2.8	2000	8	ADA71938	Ada71938 Rice gene	

ALIGNMENTS

RESULT 1
AAN92440

SCORE Search Results Details for Application 10606302 and Search Result us-10-606-302a-10.rge.

Score Home	Retrieve Application	SCORE System	SCORE	Comments /
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This page gives you Search Results detail for the Application 10606302 and Search Result us-10-606-302a-10.rge.

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OM nucleic - nucleic search, using sw model

```
Run on:      August 15, 2006, 09:51:39 ; Search time 12121 Seconds
              (without alignments)
              11184.560 Million cell updates/sec
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```
Title:          US-10-606-302A-10
Perfect score:  2120
Sequence:       1 ggatcctcctgatcactgga.....accaagatgttcagctacc 2120
```

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 6366136 seqs, 31973710525 residues

Total number of hits satisfying chosen parameters: 12732272

```
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
```

```
Post-processing: Minimum Match 0%
                  Maximum Match 100%
                  Listing first 45 summaries
```

```
Database : GenEmbl:*
1: gb_env:*
2: gb_pat:*
3: gb_ph:*
4: gb_pl:*
5: gb_pr:*
6: gb_ro:*
7: gb_sts:*
8: gb_sy:*
9: gb_un:*
10: gb_vi:*
11: gb_ov:*
12: gb_htg:*
13: gb_in:*
14: gb_om:*
15: gb_ba:*
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	2120	100.0	2120	2	CS017724	CS017724 Sequence
2	2120	100.0	2120	2	E01923	E01923 cDNA encodi
3	2120	100.0	2120	2	AR405969	AR405969 Sequence
4	2120	100.0	2120	2	AX374957	AX374957 Sequence
5	2120	100.0	2120	6	RATFLAVIN	J03536 Rat L-gulon
6	2087.6	98.5	2192	6	BC089803	BC089803 Rattus no
7	1565.6	73.8	2240	6	BC028828	BC028828 Mus muscu
8	1564	73.8	2227	6	BC019856	BC019856 Mus muscu
9	1564	73.8	2235	6	BC028822	BC028822 Mus muscu
10	1475.4	69.6	2035	6	BC034835	BC034835 Mus muscu
11	1323	62.4	1323	2	AX402018	AX402018 Sequence
12	1319.8	62.3	1323	2	A93824	A93824 Sequence 3
13	1188.6	56.1	1323	6	AY453064	AY453064 Mus muscu
14	1058.6	49.9	1939	14	AF440259	AF440259 Sus scrof
15	1031.2	48.6	2127	14	BC102936	BC102936 Bos tauru
16	879.8	41.5	6009	6	D12754	D12754 Rattus norv
c 17	879.8	41.5	239102	12	AC137051	AC137051 Rattus no
18	879.8	41.5	267809	12	AC137461	AC137461 Rattus no
19	714.2	33.7	1976	11	BC084892	BC084892 Xenopus l
20	642.2	30.3	1747	11	AY039838	AY039838 Scyliorhi
21	592	27.9	688	2	AX525572	AX525572 Sequence
c 22	480.2	22.7	141017	6	AC126444	AC126444 Mus muscu
c 23	480.2	22.7	191606	6	AC126272	AC126272 Mus muscu
24	473.8	22.3	605	14	AF185292	AF185292 Bos tauru
25	441	20.8	847	11	BX933840	BX933840 Gallus ga
26	329	15.5	727	11	BX934260	BX934260 Gallus ga
c 27	324	15.3	384	2	AX400983	AX400983 Sequence
28	321.2	15.2	661	6	BC035221	BC035221 Mus muscu
29	290.6	13.7	2095	13	AK115232	AK115232 Ciona int
30	177.2	8.4	110000	15	CP000088_22	Continuation (23 o
c 31	169	8.0	201	2	AX309322	AX309322 Sequence
32	164.6	7.8	110000	15	BA000030_29	Continuation (30 o
c 33	162	7.6	295150	15	SCO939125	AL939125 Streptomy
34	156.8	7.4	167	2	CQ435909	CQ435909 Sequence
c 35	150.2	7.1	110000	15	CP000249_03	Continuation (4 of
c 36	150.2	7.1	110000	15	CP000249_04	Continuation (5 of
c 37	142.4	6.7	190294	12	AC158696	AC158696 Bos tauru
38	142.4	6.7	270496	12	AC163911	AC163911 Bos tauru
39	134.8	6.4	190294	12	AC158696	AC158696 Bos tauru
40	134.4	6.3	4612	6	D12762	D12762 Cavia porce
41	134	6.3	158	14	AF136938	AF136938 Sus scrof
c 42	133.6	6.3	110000	4	AE016819_12	Continuation (13 o
43	121.8	5.7	110000	15	AP006618_46	Continuation (47 o
44	120.4	5.7	1284	2	AR456097	AR456097 Sequence
45	120.4	5.7	110000	15	AE000516_19	Continuation (20 o

ALIGNMENTS

RESULT 1
CS017724

SCORE Search Results Details for Application 10606302 and Search Result us-10-606-302a-8.rst.

Score Home Page	Retrieve Application List	SCORE System Overview	SCORE FAQ	Comments / Suggestions
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OM nucleic - nucleic search, using sw model

Run on: August 15, 2006, 10:05:07 ; Search time 9129.93 Seconds
 (without alignments)
 13094.897 Million cell updates/sec

Title: US-10-606-302A-8
 Perfect score: 2138
 Sequence: 1 cccatgtctactatcccatt.....aaaatggtagaatcgtggtc 2138

Scoring table: IDENTITY_NUC
 Gapop 10.0 , Gapext 1.0

Searched: 48236798 seqs, 27959665780 residues

Total number of hits satisfying chosen parameters: 96473596

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : EST:*

- 1: gb_est1:*
- 2: gb_est3:*
- 3: gb_est4:*
- 4: gb_est5:*
- 5: gb_est6:*
- 6: gb_htc:*
- 7: gb_est2:*
- 8: gb_est7:*
- 9: gb_est8:*
- 10: gb_est9:*
- 11: gb_gss1:*
- 12: gb_gss2:*
- 13: gb_gss3:*
- 14: gb_gss4:*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result	No.	Score	% Query Match	Length	DB	ID	Description

	1	457.6	21.4	961	14	CNS06DEH	AL393711 T7 end of
c	2	323.2	15.1	1098	14	CNS06LXM	AL404768 T3 end of
	3	304.8	14.3	1084	14	CNS076UF	AL431869 T7 end of
c	4	282.6	13.2	553	11	BZ305138	BZ305138 KD3345.q1
	5	133.2	6.2	869	10	DR640257	DR640257 EST103088
	6	126.8	5.9	972	10	DR634104	DR634104 EST102472
c	7	121.8	5.7	940	14	CNS06H1S	AL398438 T3 end of
	8	108.8	5.1	1005	14	CNS07050	AL423202 T7 end of
	9	93.4	4.4	581	11	BZ301673	BZ301673 KD1411.p1
	10	82.4	3.9	927	1	AL667095	AL667095 AL667095
	11	75.6	3.5	728	2	BI145731	BI145731 602909885
	12	75.4	3.5	2247	6	AK167460	AK167460 Mus muscu
	13	75.4	3.5	2269	6	AK077740	AK077740 Mus muscu
	14	75.2	3.5	886	5	CF551083	CF551083 AGENCOURT
	15	74.8	3.5	671	3	BW342883	BW342883 BW342883
	16	74	3.5	792	8	CO425730	CO425730 UI-M-HU0-
	17	74	3.5	808	8	CO573278	CO573278 AGENCOURT
	18	74	3.5	872	4	CA752105	CA752105 UI-M-FD0-
	19	74	3.5	886	3	BQ946437	BQ946437 AGENCOURT
	20	73.6	3.4	808	4	CB558176	CB558176 AGENCOURT
c	21	73.4	3.4	588	3	BU698006	BU698006 LL2in1000
	22	73.4	3.4	815	3	BU904729	BU904729 AGENCOURT
	23	73.2	3.4	840	4	CB559648	CB559648 AGENCOURT
c	24	72.4	3.4	514	3	BU698976	BU698976 LL2in1424
	25	72.4	3.4	935	8	CV437826	CV437826 EST891739
c	26	72	3.4	570	3	BU695653	BU695653 LL2in1199
	27	71.6	3.3	886	8	CN240306	CN240306 EST006166
c	28	71.4	3.3	537	3	BU697932	BU697932 LL2in1415
	29	71.2	3.3	878	4	CB559873	CB559873 AGENCOURT
	30	71.2	3.3	907	5	CD791363	CD791363 EST662724
	31	70.8	3.3	734	5	CF521421	CF521421 AGENCOURT
	32	70.8	3.3	797	1	AI097875	AI097875 ue40h10.y
c	33	70	3.3	674	3	BU699086	BU699086 LL2in1283
	34	70	3.3	754	5	CF519846	CF519846 AGENCOURT
	35	69.6	3.3	753	5	CF521358	CF521358 AGENCOURT
	36	69.6	3.3	907	3	BU904429	BU904429 AGENCOURT
	37	68.6	3.2	716	1	AI573803	AI573803 uj65h10.y
c	38	68.6	3.2	1101	14	CNS00EVL	AL069706 Drosophil
	39	68.2	3.2	641	7	AV976012	AV976012 AV976012
	40	67.8	3.2	760	8	CO565622	CO565622 AGENCOURT
	41	66.6	3.1	821	4	CA788084	CA788084 AGENCOURT
	42	66.4	3.1	719	2	BI146400	BI146400 602910767
	43	66.4	3.1	831	8	CO567345	CO567345 AGENCOURT
	44	66.4	3.1	867	2	BI218342	BI218342 602937723
	45	66.4	3.1	1036	7	BF533289	BF533289 602073744

ALIGNMENTS

RESULT 1
CNS06DEH
LOCUS

CNS06DEH

961 bp

DNA

linear

GSS 17-JUN-2001

SCORE Search Results Details for Application 10606302 and Search Result us-10-606-302a- 8.rnpbn.

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[start](#)

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OM nucleic - nucleic search, using sw model

Run on: August 15, 2006, 14:38:19 ; Search time 397.172 Seconds
(without alignments)
8548.706 Million cell updates/sec

Title: US-10-606-302A-8
Perfect score: 2138
Sequence: 1 cccatgtctactatcccatt.....aaaatggtagaatcgtgggc 2138

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2200221 seqs, 794037843 residues

Total number of hits satisfying chosen parameters: 4400442

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_NA_New:*

- 1: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09_NEW_PUB.seq:*
- 2: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US06_NEW_PUB.seq:*
- 3: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US07_NEW_PUB.seq:*
- 4: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US08_NEW_PUB.seq:*
- 5: /EMC_Celerra_SIDS3/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
- 6: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10_NEW_PUB.seq:*
- 7: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11_NEW_PUB.seq:*
- 8: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11_NEW_PUB.seq1:*
- 9: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11_NEW_PUB.seq2:*
- 10: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US60_NEW_PUB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query		Length	DB	ID	Description
		Match					
1	1571.4	73.5		1581	8	US-11-217-529-77873	Sequence 77873, A
2	1200.2	56.1		1581	8	US-11-217-529-1906	Sequence 1906, Ap
3	132	6.2		939	8	US-11-217-529-77872	Sequence 77872, A
4	80.8	3.8		939	8	US-11-217-529-1905	Sequence 1905, Ap
5	60.2	2.8		668	6	US-10-488-619-2085	Sequence 2085, Ap
6	49.4	2.3		7432	6	US-10-517-441-524	Sequence 524, App
7	48.8	2.3		2987	6	US-10-517-441-345	Sequence 345, App
8	48.6	2.3		16842	6	US-10-517-441-575	Sequence 575, App
c 9	48	2.2		34088	8	US-11-266-748A-23848	Sequence 23848, A
10	47.4	2.2		15355	6	US-10-517-441-689	Sequence 689, App
11	47.4	2.2		106234	8	US-11-266-748A-24973	Sequence 24973, A
12	47.2	2.2		2987	6	US-10-517-441-619	Sequence 619, App
13	47	2.2		17897	6	US-10-517-441-618	Sequence 618, App
14	46	2.2		2501	6	US-10-517-441-562	Sequence 562, App
15	46	2.2		2501	6	US-10-517-441-609	Sequence 609, App
c 16	45.8	2.1		4928	9	US-11-218-305-3816	Sequence 3816, Ap
17	45.8	2.1		6731	6	US-10-517-441-473	Sequence 473, App
18	45.8	2.1		15355	6	US-10-517-441-415	Sequence 415, App
19	44.6	2.1		7432	6	US-10-517-441-250	Sequence 250, App
20	44.4	2.1		2501	6	US-10-517-441-335	Sequence 335, App
21	44.4	2.1		12610	6	US-10-517-441-441	Sequence 441, App
22	44.4	2.1		12610	6	US-10-517-441-715	Sequence 715, App
23	44.2	2.1		6731	6	US-10-517-441-747	Sequence 747, App
24	43.8	2.0		3155	6	US-10-517-441-682	Sequence 682, App
c 25	43.6	2.0		1000	8	US-11-266-748A-199354	Sequence 199354,
c 26	43.4	2.0		1000	8	US-11-266-748A-281383	Sequence 281383,
27	43.4	2.0		1000	8	US-11-266-748A-308023	Sequence 308023,
28	42.8	2.0		2501	6	US-10-517-441-288	Sequence 288, App
29	42.8	2.0		3371	9	US-11-218-305-15348	Sequence 15348, A
30	42.8	2.0		24976	6	US-10-539-228-18	Sequence 18, Appl
c 31	42.6	2.0		4538	9	US-11-218-305-22781	Sequence 22781, A
c 32	42.4	2.0		1791	9	US-11-218-305-6944	Sequence 6944, Ap
c 33	42.4	2.0		9859	6	US-10-517-441-729	Sequence 729, App
34	42.2	2.0		156655	8	US-11-266-748A-24308	Sequence 24308, A
35	42.2	2.0		687411	6	US-10-540-898-26	Sequence 26, Appl
c 36	42	2.0		2343	9	US-11-218-305-18431	Sequence 18431, A
c 37	42	2.0		175603	6	US-10-540-898-531	Sequence 531, App
38	41.8	2.0		19634	6	US-10-517-441-687	Sequence 687, App
39	41.8	2.0		131546	8	US-11-266-748A-60109	Sequence 60109, A
c 40	41.6	1.9		402	9	US-11-348-413-12204	Sequence 12204, A
41	41.4	1.9		17897	6	US-10-517-441-617	Sequence 617, App
42	41.2	1.9		825	9	US-11-218-305-1766	Sequence 1766, Ap
c 43	41.2	1.9		1503	6	US-10-374-780A-615	Sequence 615, App
c 44	41.2	1.9		9859	6	US-10-517-441-455	Sequence 455, App
45	41.2	1.9		121124	6	US-10-540-898-83	Sequence 83, Appl

ALIGNMENTS

RESULT 1

US-11-217-529-77873

; Sequence 77873, Application US/11217529

; Publication No. US20060099612A1

; GENERAL INFORMATION:

; APPLICANT: SUNTORY LIMITED

; APPLICANT: NAKAO, YOSHIHIRO

SCORE Search Results Details for Application 10606302 and Search Result us-10-606-302a 8.rnpbm.

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[start](#)

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OM nucleic - nucleic search, using sw model

Run on: August 15, 2006, 13:10:24 ; Search time 2681.29 Seconds
(without alignments)
9797.893 Million cell updates/sec

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Gapop 10.0 , Gapext 1.0

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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SUMMARIES

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	3	1576.2	73.7	1581	9	US-10-606-300-6	Sequence 6, Appli
	4	1576.2	73.7	1581	10	US-10-606-302-6	Sequence 6, Appli
	5	1571.4	73.5	1581	11	US-10-932-182A-77873	Sequence 77873, A
	6	1200.2	56.1	1581	11	US-10-932-182A-1906	Sequence 1906, Ap
	7	132	6.2	939	11	US-10-932-182A-77872	Sequence 77872, A
	8	128.8	6.0	939	7	US-10-369-493-25534	Sequence 25534, A
	9	80.8	3.8	939	11	US-10-932-182A-1905	Sequence 1905, Ap
	10	73.8	3.5	1323	3	US-09-917-800A-1694	Sequence 1694, Ap
	11	73.8	3.5	2120	9	US-10-606-300-10	Sequence 10, Appl
	12	73.8	3.5	2120	10	US-10-606-302-10	Sequence 10, Appl
	13	57.4	2.7	13326	7	US-10-311-455-1685	Sequence 1685, Ap
	14	54	2.5	24259	8	US-10-221-714A-415	Sequence 415, App
c	15	53	2.5	1830	9	US-10-706-635-67	Sequence 67, Appl
	16	53	2.5	32392	9	US-10-706-635-27	Sequence 27, Appl
	17	52.2	2.4	16258	8	US-10-257-166-120	Sequence 120, App
c	18	52	2.4	415	12	US-10-301-480-48201	Sequence 48201, A
c	19	52	2.4	415	12	US-10-301-480-661610	Sequence 661610,
	20	51.8	2.4	8607	8	US-10-240-589C-112	Sequence 112, App
	21	51.8	2.4	8607	10	US-10-240-708-72	Sequence 72, Appl
	22	51	2.4	7903	6	US-10-239-676-110	Sequence 110, App
	23	51	2.4	7903	7	US-10-311-455-1336	Sequence 1336, Ap
	24	51	2.4	7903	7	US-10-240-453-122	Sequence 122, App
	25	50.6	2.4	11976	7	US-10-311-455-567	Sequence 567, App
	26	50.4	2.4	6917	7	US-10-311-455-2207	Sequence 2207, Ap
	27	50.2	2.3	640681	3	US-09-790-988-1	Sequence 1, Appli
	28	49.8	2.3	3673778	7	US-10-312-841-1	Sequence 1, Appli
	29	49.6	2.3	33053	8	US-10-433-793-36	Sequence 36, Appl
	30	49.6	2.3	3673778	7	US-10-312-841-2	Sequence 2, Appli
c	31	49.4	2.3	11296	7	US-10-311-455-695	Sequence 695, App
	32	49.2	2.3	6115	7	US-10-311-455-1774	Sequence 1774, Ap
	33	49.2	2.3	9524	7	US-10-311-455-812	Sequence 812, App
	34	49.2	2.3	9524	8	US-10-257-166-76	Sequence 76, Appl
	35	49.2	2.3	17213	7	US-10-311-455-1455	Sequence 1455, Ap
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c	37	49	2.3	775	12	US-10-301-480-555584	Sequence 555584,
c	38	49	2.3	775	12	US-10-301-480-1168993	Sequence 1168993,
	39	49	2.3	5503	8	US-10-257-166-104	Sequence 104, App
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c	41	49	2.3	17594	7	US-10-311-455-2000	Sequence 2000, Ap
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	43	48.8	2.3	5987	8	US-10-433-793-131	Sequence 131, App
	44	48.8	2.3	6352	8	US-10-221-613-195	Sequence 195, App
c	45	48.8	2.3	69081	6	US-10-087-192-1192	Sequence 1192, Ap

ALIGNMENTS

RESULT 1

US-10-606-300-8

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OM nucleic - nucleic search, using sw model

Run on: August 15, 2006, 11:29:45 ; Search time 280.179 Seconds
(without alignments)
14278.103 Million cell updates/sec

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Maximum Match 100%
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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	3	334.2	15.6	1185	3	US-09-248-796A-3166	Sequence 3166, Ap
	4	73.8	3.5	2120	3	US-09-630-983A-10	Sequence 10, Appl
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	6	53	2.5	1141	3	US-09-806-708B-22	Sequence 22, Appl
c	7	53	2.5	1830	3	US-09-662-254B-67	Sequence 67, Appl
	8	53	2.5	32392	3	US-09-662-254B-27	Sequence 27, Appl
	9	51	2.4	298336	3	US-09-949-016-16600	Sequence 16600, A
	10	50.2	2.3	640681	3	US-09-790-988-1	Sequence 1, Appli
	11	48.6	2.3	150032	3	US-09-949-016-14321	Sequence 14321, A
	12	48.4	2.3	1833	3	US-09-630-983A-2	Sequence 2, Appli
c	13	48	2.2	36242	3	US-09-949-016-12996	Sequence 12996, A
c	14	48	2.2	36242	3	US-09-949-016-12997	Sequence 12997, A
c	15	48	2.2	36242	3	US-09-949-016-12998	Sequence 12998, A
c	16	48	2.2	36242	3	US-09-949-016-12999	Sequence 12999, A
c	17	48	2.2	36242	3	US-09-949-016-13000	Sequence 13000, A
	18	47.8	2.2	2034	3	US-09-423-468A-12	Sequence 12, Appl
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	21	47.4	2.2	96845	3	US-09-949-016-13658	Sequence 13658, A
c	22	46.4	2.2	23501	3	US-09-949-016-17517	Sequence 17517, A
c	23	45.8	2.1	3906	3	US-09-662-254B-60	Sequence 60, Appl
c	24	45.8	2.1	50000	3	US-09-662-254B-26	Sequence 26, Appl
c	25	45.4	2.1	601	3	US-09-949-016-179398	Sequence 179398,
	26	45.4	2.1	832	3	US-09-621-976-2813	Sequence 2813, Ap
c	27	45.4	2.1	1359	3	US-09-543-681A-3702	Sequence 3702, Ap
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c	31	45.4	2.1	266293	3	US-09-949-016-11934	Sequence 11934, A
	32	45.2	2.1	87629	3	US-09-949-016-15262	Sequence 15262, A
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c	36	44.8	2.1	65485	3	US-09-949-016-13757	Sequence 13757, A
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	44	44.2	2.1	53332	3	US-10-786-065-3	Sequence 3, Appli
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ALIGNMENTS

RESULT 1

US-09-630-983A-8

; Sequence 8, Application US/09630983A

; Patent No. 6630330

; GENERAL INFORMATION:

; APPLICANT: Porro, Danilo

; APPLICANT: Sauer, Michael

; TITLE OF INVENTION: Ascorbic Acid Production from Yeast

; FILE REFERENCE: 2028.594000

; CURRENT APPLICATION NUMBER: US/09/630,983A

SCORE Search Results Details for Application 10606302 and Search Result us-10-606-302a-8.rng.

Score Home	Retrieve Application	SCORE System	SCORE	Comments./
Page	List	Overview	FAQ	Suggestions

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OM nucleic - nucleic search, using sw model

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Run on:      August 15, 2006, 09:24:26 ; Search time 1205.07 Seconds
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SUMMARIES

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3	1576.2	73.7	1581	6	ABK10122	Abk10122 Yeast cDN
4	190.6	8.9	713	6	ABL60142	Abl60142 Fungi str
5	128.8	6.0	939	13	ADS47104	Ads47104 Bacterial
6	75.4	3.5	1323	2	AAT87005	Aat87005 DNA encod
7	73.8	3.5	1323	6	ABK63787	Abk63787 Rat seque
8	73.8	3.5	1323	10	ADB58424	Adb58424 Toxicity-
9	73.8	3.5	1323	10	ADB53007	Adb53007 Primary r
10	73.8	3.5	1323	13	ADT71411	Adt71411 Rat L-gul
11	73.8	3.5	2120	1	AAN92440	Aan92440 DNA seque
12	73.8	3.5	2120	6	ABK10124	Abk10124 Rat cDNA
13	60.2	2.8	668	10	ADD34307	Add34307 Mouse mit
14	57.4	2.7	13326	6	ABL33712	Abl33712 Human imm
15	54.4	2.5	2000	11	ACL35363	Acl35363 Rice stre
16	54	2.5	2000	8	ADA71938	Ada71938 Rice gene
17	54	2.5	24259	4	AAS46691	Aas46691 Tumour su
c 18	53	2.5	1830	6	ABL56243	Abl56243 AmEPV met
19	53	2.5	32392	6	ABL56203	Abl56203 AmEPV gen
20	52.2	2.4	16258	6	ABK40038	Abk40038 Human che
21	52.2	2.4	16258	6	ABL70376	Abl70376 Chemicall
c 22	51.8	2.4	252	3	AAZ94802	Aaz94802 Soybean m
23	51.8	2.4	8607	6	ABL92303	Abl92303 Chemicall
24	51.8	2.4	8607	6	ABL49372	Abl49372 Human pol
25	51.6	2.4	8447	6	ABN80093	Abn80093 Human che
c 26	51.2	2.4	9789	2	AAT41852	Aat41852 cDNA enco
27	51	2.4	7903	4	AAS45403	Aas45403 Chemicall
28	51	2.4	7903	6	ABL33363	Abl33363 Human imm
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31	50.4	2.4	6917	6	ABL34234	Abl34234 Human imm
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34	50	2.3	6467	6	ABN80168	Abn80168 Human che
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c 37	49.6	2.3	19965	6	ABK69932	Abk69932 Human sec
38	49.6	2.3	33053	6	ABQ67006	Abq67006 Human ang
39	49.4	2.3	7432	10	ADB54208	Adb54208 Pretreate
40	49.4	2.3	7432	13	ADS89508	Ads89508 Oligonucl
c 41	49.4	2.3	11296	6	ABL32722	Abl32722 Human imm
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43	49.2	2.3	9524	6	ABK39994	Abk39994 Human che
44	49.2	2.3	9524	6	ABL32839	Abl32839 Human imm
45	49.2	2.3	17213	6	ABL33482	Abl33482 Human imm

ALIGNMENTS

RESULT 1
ABK10123

SCORE Search Results Details for Application 106

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start

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OM nucleic - nucleic search, using sw model

Run on: August 15, 2006, 09:51:39 ; Search time 12224 Seconds
(without alignments)
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Post-processing: Minimum Match 0%
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	2138	100.0	2138	4	AB009401	AB009401 Saccharom
c 5	2074.4	97.0	32148	4	SC9725	Z46660 S.cerevisia
6	1967.6	92.0	2622	4	SCU40390	U40390 Saccharomyc
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10	1576.2	73.7	1581	2	AX374953	AX374953 Sequence
11	1576.2	73.7	1581	4	AY693120	AY693120 Saccharom
12	768.4	35.9	110000	4	CR382123_14	Continuation (15 o
c 13	756.6	35.4	110000	4	CR380954_03	Continuation (4 of
c 14	619.8	29.0	110000	4	AE016819_12	Continuation (13 o
15	402.6	18.8	3762	4	AF031228	AF031228 Candida a
16	334.2	15.6	1185	2	AR548035	AR548035 Sequence
c 17	317	14.8	110000	4	CR382133_02	Continuation (3 of
c 18	294.2	13.8	103261	4	CR382127_22	Continuation (23 o
19	190.6	8.9	713	2	AX461040	AX461040 Sequence
20	128.8	6.0	939	8	DQ331123	DQ331123 Synthetic
21	119.6	5.6	110000	4	AP007151_32	Continuation (33 o
22	107.2	5.0	110000	15	BA000028_17	Continuation (18 o
c 23	105.4	4.9	36484	4	SPAPB1A10	AL512562 S.pombe c
24	84	3.9	2095	13	AK115232	AK115232 Ciona int
25	80.4	3.8	1747	11	AY039838	AY039838 Scyliorhi
c 26	78	3.6	105521	12	AC121064	AC121064 Magnaport
27	77	3.6	2192	6	BC089803	BC089803 Rattus no
28	75.4	3.5	1323	2	A93824	A93824 Sequence 3
29	75.4	3.5	1323	6	AY453064	AY453064 Mus muscu
30	75.4	3.5	2235	6	BC028822	BC028822 Mus muscu
31	75.4	3.5	2240	6	BC028828	BC028828 Mus muscu
32	73.8	3.5	1323	2	AX402018	AX402018 Sequence
33	73.8	3.5	2120	2	CS017724	CS017724 Sequence
34	73.8	3.5	2120	2	E01923	E01923 cDNA encodi
35	73.8	3.5	2120	2	AR405969	AR405969 Sequence
36	73.8	3.5	2120	2	AX374957	AX374957 Sequence
37	73.8	3.5	2120	6	RATFLAVIN	J03536 Rat L-gulon
38	73.8	3.5	2227	6	BC019856	BC019856 Mus muscu
39	71.6	3.3	1976	11	BC084892	BC084892 Xenopus l
40	69.6	3.3	2023	4	AB024527	AB024527 Nicotiana
41	68.8	3.2	110000	15	AE016877_06	Continuation (7 of
42	68.6	3.2	1951	4	AB048530	AB048530 Nicotiana
43	67.8	3.2	2127	14	BC102936	BC102936 Bos tauru
c 44	64.4	3.0	110000	12	PFMAL8P1_06	Continuation (7 of
c 45	63.4	3.0	206154	11	BX465837	BX465837 Zebrafish

ALIGNMENTS

RESULT 1

CS017722

LOCUS CS017722 2138 bp DNA linear PAT 15-FEB-2005

DEFINITION Sequence 8 from Patent EP1498489.

ACCESSION CS017722

VERSION CS017722.1 GI:59891083

KEYWORDS .

SOURCE Saccharomyces cerevisiae (baker's yeast)